```
          9          18          27          36          45          54
CTC GAG ATG CAG AGG AAC CTG GGA GCT GTG CTG GGG ATT CTG TGG GTG CAG ATT [SEQ ID NO: 1]
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 L   E   M   Q   R   N   L   G   A   V   L   G   I   L   W   V   Q   I [SEQ ID NO: 2]

          63          72          81          90          99         108
TGC TGG CTG AAA GAA CAG CAA GTG CAG CAG AGT CCC GCA TCC TTG GTT CTG CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 C   W   L   K   E   Q   Q   V   Q   Q   S   P   A   S   L   V   L   Q

         117         126         135         144         153         162
GAG GGG GAG AAC GCA GAG CTC CAG TGT AGC TTT TCC ATC TTT ACA AAC CAG GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   G   E   N   A   E   L   Q   C   S   F   S   I   F   T   N   Q   V

         171         180         189         198         207         216
CAG TGG TTT TAC CAA CGT CCT GGG GGA AGA CTC GTC AGC CTG TTG TAC AAT CCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Q   W   F   Y   Q   R   P   G   G   R   L   V   S   L   L   Y   N   P

         225         234         243         252         261         270
TCT GGG ACA AAG CAG AGT GGG AGA CTG ACA TCC ACA ACA GTC ATT AAA GAA CGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   G   T   K   Q   S   G   R   L   T   S   T   T   V   I   K   E   R

         279         288         297         306         315         324
CGC AGC TCT TTG CAC ATT TCC TCC TCC CAG ATC ACA GAC TCA GGC ACT TAT CTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 R   S   S   L   H   I   S   S   S   Q   I   T   D   S   G   T   Y   L
```

FIG. 3A

```
       333        342        351        360        369        378
TGT GCC TCA AAT TCT GGA GGA AGC AAT GCA AAG CTA ACC TTC GGG AAA GGC ACT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 C   A   S   N   S   G   G   S   N   A   K   L   T   F   G   K   G   T

       387        396        405        414        423        432
AAA CTC TCT GTT AAA TCA GGT GGC GGA GGG TCT GGC GGG GGT GGA TCC GGG GGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 K   L   S   V   K   S   G   G   G   G   S   G   G   G   G   S   G   G

       441        450        459        468        477        486
GGA GGC TCA GAG GCT GCA GTC ACC CAA AGC CCA AGA AAC AAG GTG GCA GTA ACA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   G   S   E   A   A   V   T   Q   S   P   R   N   K   V   A   V   T

       495        504        513        522        531        540
GGA GGA AAG GTG ACA TTG AGC TGT AAT CAG ACT AAT AAC CAC AAC AAC ATG TAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   G   K   V   T   L   S   C   N   Q   T   N   N   H   N   N   M   Y

       549        558        567        576        585        594
TGG TAT CGG CAG GAC ACG GGG CAT GGG CTG AGG CTG ATC CAT TAT TCA TAT GGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 W   Y   R   Q   D   T   G   H   G   L   R   L   I   H   Y   S   Y   G

       603        612        621        630        639        648
GCT GGC AGC ACT GAG AAA GGA GAT ATC CCT GAT GGA TAC AAG GCC TCC AGA CCA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 A   G   S   T   E   K   G   D   I   P   D   G   Y   K   A   S   R   P
```

FIG. 3B

```
        657         666         675         684         693         702
AGC CAA GAG AAC TTC TCC CTC ATT CTG GAG TTG GCT ACC CCC TCT CAG ACA TCA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   Q   E   N   F   S   L   I   L   E   L   A   T   P   S   Q   T   S

        711         720         729         738         747         756
GTG TAC TTC TGT GCC AGC GGT GAG ACA GGG ACC AAC GAA AGA TTA TTT TTC GGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   Y   F   C   A   S   G   E   T   G   T   N   E   R   L   F   F   G

        765         774         783         792         801         810
CAT GGA ACC AAG CTG TCT GTC CTG ACT AGT AAC TCC ATC ATG TAC TTC AGC CAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   G   T   K   L   S   V   L   T   S   N   S   I   M   Y   F   S   H

        819         828         837         846         855         864
TTC GTG CCG GTC TTC CTG CCA GCG AAG CCC ACC ACG ACG CCA GCG CCG CGA CCA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 F   V   P   V   F   L   P   A   K   P   T   T   T   P   A   P   R   P

        873         882         891         900         909         918
CCA ACA CCG GCG CCC ACC ATC GCG TCG CAG CCC CTG TCC CTG CGC CCA TCT AGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   T   P   A   P   T   I   A   S   Q   P   L   S   L   R   P   S   S

        927         936         945         954         963         972
TCT AGA GAT CCC AAA CTC TGC TAC CTG CTG GAT GGA ATC CTC TTC ATC TAT GGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   R   D   P   K   L   C   Y   L   L   D   G   I   L   F   I   Y   G
```

FIG. 3C

```
      981        990        999       1008       1017       1026
GTC ATT CTC ACT GCC TTG TTC CTG AGA GTG AAG TTC AGC AGG AGC GCA GAC GCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   I   L   T   A   L   F   L   R   V   K   F   S   R   S   A   D   A

     1035       1044       1053       1062       1071       1080
CCC GCG TAC CAG CAG GGC CAG AAC CAG CTC TAT AAC GAG CTC AAT CTA GGA CGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   A   Y   Q   Q   G   Q   N   Q   L   Y   N   E   L   N   L   G   R

     1089       1098       1107       1116       1125       1134
AGA GAG GAG TAC GAT GTT TTG GAC AAG AGA CGT GGC CGG GAC CCT GAG ATG GGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 R   E   E   Y   D   V   L   D   K   R   R   G   R   D   P   E   M   G

     1143       1152       1161       1170       1179       1188
GGA AAG CCG AGA AGG AAG AAC CCT CAG GAA GGC CTG TAC AAT GAA CTG CAG AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   K   P   R   R   K   N   P   Q   E   G   L   Y   N   E   L   Q   K

     1197       1206       1215       1224       1233       1242
GAT AAG ATG GCG GAG GCC TAC AGT GAG ATT GGG ATG AAA GGC GAG CGC CGG AGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 D   K   M   A   E   A   Y   S   E   I   G   M   K   G   E   R   R   R

     1251       1260       1269       1278       1287       1296
GGC AAG GGG CAC GAT GGC CTT TAC CAG GGT CTC AGT ACA GCC ACC AAG GAC ACC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 G   K   G   H   D   G   L   Y   Q   G   L   S   T   A   T   K   D   T

     1305       1314       1323       1332
TAC GAC GCC CTT CAC ATG CAG GCC CTG CCC CCT CGC TAA
--- --- --- --- --- --- --- --- --- --- --- --- ---
 Y   D   A   L   H   M   Q   A   L   P   P   R   *
```

FIG. 3D

```
          9          18          27          36          45          54
ATG AAA TCC TTG AGT GTT TCC CTA GTG GTC CTG TGG CTC CAG TTA AAC TGG GTG   [SEQ ID NO: 43]
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Met Lys Ser Leu Ser Val Ser Leu Val Val Leu Trp Leu Gln Leu Asn Trp Val   [SEQ ID NO: 44]

          63          72          81          90          99         108
CAG AGC CAG CAG AAG GTG CAG CAG AGC CCA GAA TCC CTC AGT GTC CCA GAG GGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser Val Pro Glu Gly

         117         126         135         144         153         162
GGC ATG GCC TCT CTC AAC TGC ACT TCA AGT GAT CGC AAT TTT CAG TAT TTC TGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg Asn Phe Gln Tyr Phe Trp

         171         180         189         198         207         216
TGG TAC AGA CAG CAT TCT GGA GAA GGC CCC AAA GCA CTG ATG TCC ATC TTC TCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Trp Tyr Arg Gln His Ser Gly Glu Gly Pro Lys Ala Leu Met Ser Ile Phe Ser
```

FIG. 7A

```
      225        234        243        252        261        270
GAT GGT GAC AAG AAA GAA GGC AGA TTC ACA GCT CAC CTC AAT AAG GCC AGC CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Asp Gly Asp Lys Lys Glu Gly Arg Phe Thr Ala His Leu Asn Lys Ala Ser Leu

      279        288        297        306        315        324
CAT GTT TCC CTG CAC ATC AGA GAC TCC CAG CCC AGT GAC TCC GCT CTC TAC TTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
His Val Ser Leu His Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe

      333        342        351        360        369        378
TGT GCA GTT ATG GAT TAT AAC CAG GGG AAG CTT ATC TTT GGG CAG GGT ACC AAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Cys Ala Val Met Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys

      387
TTA TCT ATC AAG CCC 3'
--- --- --- --- ---
Leu Ser Ile Lys Pro
```

FIG. 7B

```
         9          18          27          36          45          54
ATG GGC TCC AGA CTC TTC TTT GTG GTT TTG ATT CTC CTG TGT GCA AAA CAC ATG   [SEQ ID NO: 45]
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Met Gly Ser Arg Leu Phe Phe Val Val Leu Ile Leu Leu Cys Ala Lys His Met   [SEQ ID NO: 46]

         63          72          81          90          99          108
GAG GCT GCA GTC ACC CAA AGT CCA AGA AGC AAG GTG GCA GTA ACA GGA GGA AAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val Thr Gly Gly Lys

        117         126         135         144         153         162
GTG ACA TTG AGC TGT CAC CAG ACT AAT AAC CAT GAC TAT ATG TAC TGG TAT CGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp Tyr Met Tyr Trp Tyr Arg

        171         180         189         198         207         216
CAG GAC ACG GGG CAT GGG CTG AGG CTG ATC CAT TAC TCA TAT GTC GCT GAC AGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Gln Asp Thr Gly His Gly Leu Arg Leu Ile His Tyr Ser Tyr Val Ala Asp Ser
```

FIG. 7C

```
        225         234         243         252         261         270
ACG GAG AAA GGA GAT ATC CCT GAT GGG TAC AAG GCC TCC AGA CCA AGC CAA GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Thr Glu Lys Gly Asp Ile Pro Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu

        279         288         297         306         315         324
AAT TTC TCT CTC ATT CTG GAG TTG GCT TCC CTT TCT CAG TCA GCT GTA TAT TTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Asn Phe Ser Leu Ile Leu Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe

        333         342         351         360         369         378
TGT GCC AGC AGC GAT TTC GCC GGG ACA GGG GGC TTC TAT GAA CAG TAC TTC GGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Cys Ala Ser Ser Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly

        387         396
CCC GGC ACC AGG CTC ACG GTT TCT 3'
--- --- --- --- --- --- --- ---
Pro Gly Thr Arg Leu Thr Val Ser
```

FIG. 7D

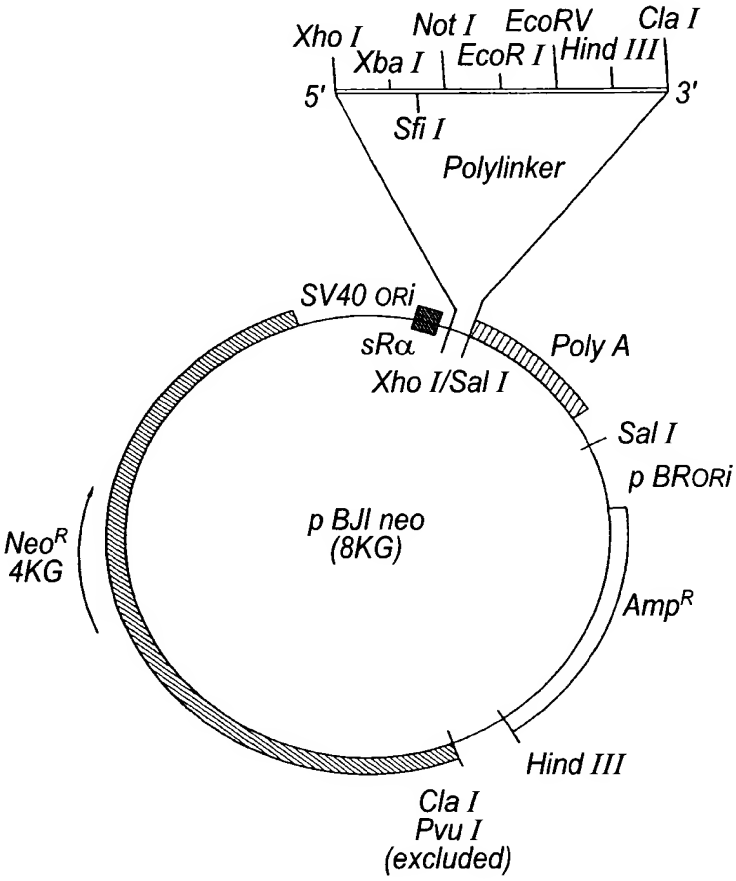

FIG. 8